

<b>Notice of References Cited</b>	<b>Application/Control No.</b> 09/736,960	<b>Applicant(s)/Patent Under Reexamination</b> LU ET AL.	
	<b>Examiner</b> Bridget E. Bunner	<b>Art Unit</b> 1647	<b>Page 1 of 3</b>

**U.S. PATENT DOCUMENTS**

*		Document Number Country Code-Number-Kind Code	Date MM-YYYY	Name	Classification
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*		Include as applicable: Author, Title Date, Publisher, Edition or Volume, Pertinent Pages)
	U	Skolnick et al. From genes to protein structure and function: novel applications of computational approaches in the genomic era. Trends in Biotech 18(1): 34-39, 2000
	V	Bork, A. Powers and pitfalls in sequence analysis: the 70% hurdle. Genome Res 10: 398-400, 2000.

\*A copy of this reference is not being furnished with this Office action. See MPEP § 701.03(a).  
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Examiner

Bridget E. Bunner

Art Unit

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	U	Brenner, S.E. Errors in genome function. Trends in Genetics 15(4): 132-133, 1999.
	V	Bork et al. Go hunting in sequence databases but watch out for the traps. Trends in Genetics. 12(10): 425-427, 1996.

1. A method for predicting the tertiary structure of a protein, comprising: (a) obtaining a protein sequence; (b) identifying a protein family to which the protein sequence belongs; (c) identifying a protein structure within the protein family; and (d) predicting the tertiary structure of the protein based on the protein structure within the protein family. pp. 492-495, 1994.

\*A copy of this reference is not being furnished with this Office action. See MPEP § 701.05 a  
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	U	Lewin, B. Genes. New York: John Wiley and Sons, Second edition, 1985, pg 681.
	V	Hegde et al. Genbank Accession No. AW959798, direct submission, EST database, 01 June 2000.

\*A copy of this reference is not being furnished with this Office action. See MPEP § 701.05.a  
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